

ABSTRACT OF THE DISCLOSURE

The present invention relates to identifying protein epitopes and more particularly to a novel method for identifying, determining the location, optimal length of amino acid residues and immunobiological potency of protein epitopes by fitting a hydrophilicity and/or hydrophobicity plot generated for the amino acid linear sequence of a polypeptide to a mathematically generated continuous curve thereby generating at least one set of potential epitopes which include ranked potential epitopes having a specific number of amino acid residues. The immunobiologically-active linear peptides are deemed the potential epitopes that exhibit the most alternating positioning about an equilibrium position when juxtaposed on the hydrophilicity and/or hydrophobicity plot and their optimal length corresponds to the specific number of amino acid residues in the set of ranked potential epitopes. The amino acid sequence of the protein epitopes of the present invention exhibit a hydrophobic-hydrophilic-hydrophobic motif.